



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/042,526  
Source: Oipe  
Date Processed by STIC: 8-4-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220-20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,526

DATE: 08/04/2004  
TIME: 10:04:39

Input Set : A:\pto.lm.txt  
Output Set: N:\CRF4\08042004\J042526.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

E--> 6 (i) APPLICANT: mandatory response needed  
8 (ii) TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine Formulations  
9 and Methods of Use

E--> 11 (iii) NUMBER OF SEQUENCES: 27 28 see pg.5

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
15 (B) STREET: 233 South Wacker Drive, 6300 Sears Tower  
16 (C) CITY: Chicago  
17 (D) STATE: Illinois  
18 (E) COUNTRY: United States of America  
19 (F) ZIP: 60606-6402

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

Does Not Comply  
Corrected Diskette Needed

27 (vi) CURRENT APPLICATION DATA:  
C--> 28 (A) APPLICATION NUMBER: US/10/042,526

C--> 29 (B) FILING DATE: 29-Apr-2002  
30 (C) CLASSIFICATION:

32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Williams Jr., Joseph A.

34 (B) REGISTRATION NUMBER: 38,659  
35 (C) REFERENCE/DOCKET NUMBER: 27013/34028

37 (ix) TELECOMMUNICATION INFORMATION:  
38 (A) TELEPHONE: 312-474-6300

39 (B) TELEFAX: 312-474-0448

## ERRORED SEQUENCES

185 (2) INFORMATION FOR SEQ ID NO: 2:

187 (i) SEQUENCE CHARACTERISTICS:

188 (A) LENGTH: 506 amino acids 505 see P.3

189 (B) TYPE: amino acid

190 (D) TOPOLOGY: linear

192 (ii) MOLECULE TYPE: protein

194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

196 Met Ser Leu Trp Leu Pro Ser Glu Ala Thr Val Tyr Leu Pro Pro Val

197 1 5 10 15

199 Pro Val Ser Lys Val Val Ser Thr Asp Glu Tyr Val Ala Arg Thr Asn

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200	20	25	30	
202	Ile Tyr Tyr His Ala Gly Thr Ser Arg Leu Leu Ala Val Gly His Pro.			
203	35	40	45	
205	Tyr Phe Pro Ile Lys Lys Pro Asn Asn Asn Lys Ile Leu Val Pro Lys			
206	50	55	60	
208	Val Ser Gly Leu Gln Tyr Arg Val Phe Arg Ile His Leu Pro Asp Pro			
209	65	70	75	80
211	Asn Lys Phe Gly Phe Pro Asp Thr Ser Phe Tyr Asn Pro Asp Thr Gln			
212	85	90	95	
214	Arg Leu Val Trp Ala Cys Val Gly Val Glu Val Gly Arg Gly Gln Pro			
215	100	105	110	
217	Leu Gly Val Gly Ile Ser Gly His Pro Leu Leu Asn Lys Leu Asp Asp			
218	115	120	125	
220	Thr Glu Asn Ala Ser Ala Tyr Ala Ala Asn Ala Gly Val Asp Asn Arg			
221	130	135	140	
223	Glu Cys Ile Ser Met Asp Tyr Lys Gln Thr Gln Leu Cys Leu Ile Gly			
224	145	150	155	160
226	Cys Lys Pro Pro Ile Gly Glu His Trp Gly Lys Gly Ser Pro Cys Thr			
227	165	170	175	
229	Asn Val Ala Val Asn Pro Gly Asp Cys Pro Pro Leu Glu Leu Ile Asn			
230	180	185	190	
232	Thr Val Ile Gln Asp Gly Asp Met Val Asp Thr Gly Phe Gly Ala Met			
233	195	200	205	
235	Asp Phe Thr Thr Leu Gln Ala Asn Lys Ser Glu Val Pro Leu Asp Ile			
236	210	215	220	
238	Cys Thr Ser Ile Cys Lys Tyr Pro Asp Tyr Ile Lys Met Val Ser Glu			
239	225	230	235	240
241	Pro Tyr Gly Asp Ser Leu Phe Phe Tyr Leu Arg Arg Glu Gln Met Phe			
242	245	250	255	
244	Val Arg His Leu Phe Asn Arg Ala Gly Ala Val Gly Glu Asn Val Pro			
245	260	265	270	
247	Asp Asp Leu Tyr Ile Lys Gly Ser Gly Ser Thr Ala Asn Leu Ala Ser			
248	275	280	285	
250	Ser Asn Tyr Phe Pro Thr Pro Ser Gly Ser Met Val Thr Ser Asp Ala			
251	290	295	300	
255	Gln Ile Phe Asn Lys Pro Tyr Trp Leu Gln Arg Ala Gln Gly His Asn			
256	305	310	315	320
258	Asn Gly Ile Cys Trp Gly Asn Gln Leu Phe Val Thr Val Val Asp Thr			
259	325	330	335	
261	Thr Arg Ser Thr Asn Met Ser Leu Cys Ala Ala Ile Ser Thr Ser Glu			
262	340	345	350	
264	Thr Thr Tyr Lys Asn Thr Asn Phe Lys Glu Tyr Leu Arg His Gly Glu			
265	355	360	365	
267	Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Lys Ile Thr Leu Thr			
268	370	375	380	
270	Ala Asp Val Met Thr Tyr Ile His Ser Met Asn Ser Thr Ile Leu Glu			
271	385	390	395	400
273	Asp Trp Asn Phe Gly Leu Gln Pro Pro Pro Gly Gly Thr Leu Glu Asp.			
274	405	410	415	

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276 Thr Tyr Arg Phe Val Thr Ser Gln Ala Ile Ala Cys Gln Lys His Thr  
277 420 425 430  
279 Pro Pro Ala Pro Lys Glu Asp Pro Leu Lys Lys Tyr Thr Phe Trp Glu  
280 435 440 445  
282 Val Asn Leu Lys Glu Lys Phe Ser Ala Asp Leu Asp Gln Phe Pro Leu  
283 450 455 460  
285 Gly Arg Lys Phe Leu Leu Gln Ala Gly Leu Lys Ala Lys Pro Lys Phe  
286 465 470 475 480  
288 Thr Leu Gly Lys Arg Lys Ala Thr Pro Thr Thr Ser Ser Thr Ser Thr  
289 485 490 495

E--> 291 Thr Ala Lys Arg Lys Arg Lys Leu \*Delete, do not count  
292 500 505 stop codon

338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 98 amino acids 97(Same)  
error

342 (B) TYPE: amino acid

343 (D) TOPOLOGY: linear

345 (ii) MOLECULE TYPE: protein

347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

349 Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
350 1 5 10 15

352 Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
353 20 25 30

355 Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
356 35 40 45

359 Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
360 50 55 60

363 Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
364 65 70 75 80

366 Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
367 85 90 95

E--> 369 Lys Pro \*Delete

583 (2) INFORMATION FOR SEQ ID NO: 18:

585 (i) SEQUENCE CHARACTERISTICS:

586 (A) LENGTH: 97 amino acids 96

587 (B) TYPE: amino acid

588 (D) TOPOLOGY: linear

590 (ii) MOLECULE TYPE: protein

592 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

594 Met Ser Leu Leu Thr Glu Val Glu Thr Leu Thr Arg Asn Gly Trp Glu  
595 1 5 10 15

597 Cys Lys Cys Ser Asp Ser Ser Asp Pro Leu Ile Ile Ala Ala Ser Ile  
598 20 25 30

601 Ile Gly Ile Leu His Leu Ile Leu Trp Ile Phe Tyr Arg Leu Phe Phe  
602 35 40 45

604 Lys Cys Ile Tyr Arg Arg Leu Lys Tyr Gly Leu Lys Arg Gly Pro Ser  
605 50 55 60

607 Thr Glu Gly Ala Pro Glu Ser Met Arg Glu Glu Tyr Arg Gln Glu Gln  
608 65 70 75 80

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Input Set : A:\pto.lm.txt  
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610 Gln Ser Ala Val Asp Val Asp Asp Val His Phe Val Asn Ile Glu Leu  
611 85 90 95  
E--> 613 Glu <sup>\*</sup>① *delete.*

(2) INFORMATION FOR SEQ ID NO:28: → last seq. in submitted file.

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATCTGAAGC TTATTGTACG CACAACCGAA GCGTAGAGTC ACACTTG

47

□

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/042,526

DATE: 08/04/2004  
TIME: 10:04:40

Input Set : A:\pto.lm.txt  
Output Set: N:\CRF4\08042004\J042526.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1) Value not provided  
L:291 M:342 E: Invalid Stop Code On Error, STOP CODON:  
L:303 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:369 M:342 E: Invalid Stop Code On Error, STOP CODON:  
L:369 M:203 E: No. of Seq. differs, LENGTH:Input:98 Found:99 SEQ:4  
L:379 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:393 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:421 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:436 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:450 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:464 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:478 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:492 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
L:506 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:520 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
L:534 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16  
L:548 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17  
L:613 M:342 E: Invalid Stop Code On Error, STOP CODON:  
L:613 M:203 E: No. of Seq. differs, LENGTH:Input:97 Found:98 SEQ:18  
L:623 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19  
L:637 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20  
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21  
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22  
L:679 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23  
L:693 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25  
L:721 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:735 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27  
L:751 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28  
L:11 M:203 E: No. of Seq. differs, : Input 27, Counted 28